CRF Errors Corrected by the STIC Systems Branch

Serial Number: O8/249,671

CRF Processing Date: 06/16/94

Edited by: ___

Verified by: ___ (STIC staff)

ENTERED

☐ Changed a file from non-ASCII to ASCII

☑ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐ Edited a format error in the Current Application Data section, specifically: ___

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other ___

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☑ Changed the spelling of a mandatory field (the headings or subheadings), specifically: Attorney/Agent Information:

☐ Inserted a space between the last nucleic designator and the nucleic number for sequences: ___

☐ Deleted page numbers in the text of the sequence listing, which is considered invalid text.

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: ___

☐ Inserted a nucleic number at the end of a nucleic line. SEQ ID NO's edited: ___

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included: ___

☐ Deleted extra, invalid, headings used by an applicant, specifically: ___

☐ Deleted non-ASCII "garbage" at the end of files, and other invalid text, such as a secretary's initials.

☐ Inserted mandatory headings, specifically: ___

☐ Corrected an obvious error in the response, specifically: ___

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically: ___

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☑ Other: Started applicant names on same line as heading

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

8/01/93

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/249,671*

DATE: 06/16/94
TIME: 16:58:10

INPUT SET: S2395.raw

CL

> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

```
 1                             SEQUENCE LISTING
 2
 3    (1)    General Information:
 4
 5         (i) APPLICANTS:        Hauptmann, R.
 6                                Falkner, E.
 7                                Bodo, G.
 8                                VoÃ, T.
 9                                Maurer- Fogy, I.
10
11       (ii) TITLE OF INVENTION:   Process for Preparing and Purifying
12                                  alpha-Interferon
13
14      (iii) NUMBER OF SEQUENCES: 12
15
16       (iv) CORRESPONDENCE ADDRESS:
17            (A) ADDRESSEE:  Sterne, Kessler, Goldstein & Fox
18            (B) STREET:  1100 New York Avenue, Suite 600
19            (C) CITY:  Washington
20            (D) STATE:  D.C.
21            (E) COUNTRY:  U.S.A.
22            (F) ZIP:  20005
23
24        (v) COMPUTER READABLE FORM:
25            (A) MEDIUM TYPE: Floppy disk
26            (B) COMPUTER: IBM PC compatible
27            (C) OPERATING SYSTEM: PC-DOS/MS-DOS
28            (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
29
30       (vi) CURRENT APPLICATION DATA:
31            (A) APPLICATION NUMBER:
32            (B) FILING DATE:  herewith
33            (C) CLASSIFICATION:
34
35     (viii) ATTORNEY/AGENT INFORMATION:
36            (A) NAME:  Esmond, Robert W. RWE/EG
37            (B) REGISTRATION NUMBER:  32,893
38            (C) REFERENCE/DOCKET NUMBER: 0652.1350000
39
40       (ix) TELECOMMUNICATION INFORMATION:
41            (A) TELEPHONE:  (202) 371-2600
42            (B) TELEFAX:  (202) 371-2540
43
44
45
46    (2) INFORMATION FOR SEQ ID NO: 1:
```

ENTERED

INPUT SET: S2395.raw

```
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48          (i)  SEQUENCE CHARACTERISTICS:
49               (A) LENGTH: 25 base pairs
50               (B) TYPE: nucleic acid
51               (C) STRANDEDNESS: both
52               (D) TOPOLOGY: unknown
53
54         (ii) MOLECULE TYPE: cDNA
55
56         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
57
58 CGTCTTCAAG AATTCGAGAT TATCG                                    25
59
60 (2) INFORMATION FOR SEQ ID NO: 2:
61
62          (i)  SEQUENCE CHARACTERISTICS:
63               (A) LENGTH: 56 base pairs
64               (B) TYPE: nucleic acid
65               (C) STRANDEDNESS: both
66               (D) TOPOLOGY: unknown
67
68         (ii) MOLECULE TYPE: cDNA
69
70
71
72         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
73
74 GACTTCAGAA GCTTCTGCAG TTACGATCGT TATCATTCCT TACTTCTTAA ACTTTC      56
75
76 (2) INFORMATION FOR SEQ ID NO: 3:
77
78          (i)  SEQUENCE CHARACTERISTICS:
79               (A) LENGTH: 35 base pairs
80               (B) TYPE: nucleic acid
81               (C) STRANDEDNESS: both
82               (D) TOPOLOGY: unknown
83
84         (ii) MOLECULE TYPE: cDNA
85
86
87
88         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
89
90 ATGCCTATGC ATGTGATCTG CCTCAAACCC ACAGC                          35
91
92 (2) INFORMATION FOR SEQ ID NO: 4:
93
94          (i)  SEQUENCE CHARACTERISTICS:
95               (A) LENGTH: 34 base pairs
96               (B) TYPE: nucleic acid
97               (C) STRANDEDNESS: both
98               (D) TOPOLOGY: unknown
99
```

```
100        (ii) MOLECULE TYPE: cDNA
101
102
103
104        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
105
106   GGCAGATCAC ATGCATAGGC ATTTGTAGCA ATAG                              34
107
108   (2) INFORMATION FOR SEQ ID NO: 5:
109
110        (i) SEQUENCE CHARACTERISTICS:
111             (A) LENGTH: 165 amino acids
112             (B) TYPE: amino acid
113             (D) TOPOLOGY: linear
114
115        (ii) MOLECULE TYPE: protein
116
117
118
119        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
120
121        Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met
122        1               5                   10                  15
123
124        Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp
125                    20                  25                  30
126
127        Arg Arg Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln
128                    35                  40                  45
129
130        Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe
131             50                  55                  60
132
133        Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu
134        65                  70                  75                  80
135
136        Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu
137                    85                  90                  95
138
139        Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Lys
140             .      100                 105                 110
141
142        Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu
143                    115                 120                 125
144
145        Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg
146             130                 135                 140
147
148        Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser
149        145                 150                 155                 160
150
151        Leu Arg Ser Lys Glu
152                    165
```

PAGE: 4

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/249,671

DATE: 06/16/94
TIME: 16:58:27

INPUT SET: S2395.raw

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154    (2) INFORMATION FOR SEQ ID NO: 6:
155
156        (i) SEQUENCE CHARACTERISTICS:
157            (A) LENGTH: 495 base pairs
158            (B) TYPE: nucleic acid
159            (C) STRANDEDNESS: both
160            (D) TOPOLOGY: unknown
161
162        (ii) MOLECULE TYPE: cDNA
163
164
165        (ix) FEATURE:
166            (A) NAME/KEY: CDS
167            (B) LOCATION: 1..495
168
169
170        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
171
172    TGT GAT CTG CCT CAA ACC CAC AGC CTG GGT AGC AGG AGG ACC TTG ATG      48
173    Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met
174     1               5                  10                  15
175
176    CTC CTG GCA CAG ATG AGG AGA ATC TCT CTT TTC TCC TGC TTG AAG GAC      96
177    Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp
178                 20                  25                  30
179
180    AGA CGT GAC TTT GGA TTT CCC CAG GAG GAG TTT GGC AAC CAG TTC CAA     144
181    Arg Arg Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln
182                 35                  40                  45
183
184    AAG GCT GAA ACC ATC CCT GTC CTC CAT GAG ATG ATC CAG CAG ATC TTC     192
185    Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe
186         50                  55                  60
187
188    AAT CTC TTC AGC ACA AAG GAC TCA TCT GCT GCT TGG GAT GAG ACC CTC     240
189    Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu
190     65                  70                  75                  80
191
192    CTA GAC AAA TTC TAC ACT GAA CTC TAC CAG CAG CTG AAT GAC CTG GAA     288
193    Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu
194                 85                  90                  95
195
196    GCC TGT GTG ATA CAG GGG GTG GGG GTG ACA GAG ACT CCC CTG ATG AAG     336
197    Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Lys
198                 100                 105                 110
199
200    GAG GAC TCC ATT CTG GCT GTG AGG AAA TAC TTC CAA AGA ATC ACT CTC     384
201    Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu
202                 115                 120                 125
203
204    TAT CTG AAA GAG AAG AAA TAC AGC CCT TGT GCC TGG GAG GTT GTC AGA     432
205    Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg
```

```
206        130                 135                 140
207
208    GCA GAA ATC ATG AGA TCT TTT TCT TTG TCA ACA AAC TTG CAA GAA AGT    480
209    Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser
210    145                 150                 155                 160
211
212    TTA AGA AGT AAG GAA                                                 495
213    Leu Arg Ser Lys Glu
214                        165
215
216
217    (2) INFORMATION FOR SEQ ID NO: 7:
218
219            (i)  SEQUENCE CHARACTERISTICS:
220                 (A) LENGTH: 165 amino acids
221                 (B) TYPE: amino acid
222                 (D) TOPOLOGY: linear
223
224        (ii) MOLECULE TYPE: protein
225
226        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
227
228    Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met
229     1               5                   10                  15
230
231    Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp
232                20                  25                  30
233
234    Arg Arg Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln
235                35                  40                  45
236
237    Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe
238        50                  55                  60
239
240    Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu
241     65                  70                  75                  80
242
243    Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu
244                85                  90                  95
245
246    Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Lys
247                100                 105                 110
248
249    Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu
250            115                 120                 125
251
252    Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg
253        130                 135                 140
254
255    Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser
256    145                 150                 155                 160
257
258    Leu Arg Ser Lys Glu
```

RAW SEQUENCE LISTING
PATENT APPLICATION   *US/08/249,671*

INPUT SET: S2395.raw

****** PREVIOUSLY ERRORED SEQUENCES - EDITED *****

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60      (2) INFORMATION FOR SEQ ID NO: 2:
61
62          (i) SEQUENCE CHARACTERISTICS:
63              (A) LENGTH: 56 base pairs
64              (B) TYPE: nucleic acid
65              (C) STRANDEDNESS: both
66              (D) TOPOLOGY: unknown
67
68         (ii) MOLECULE TYPE: cDNA
69
70
71
72         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
73
74   GACTTCAGAA GCTTCTGCAG TTACGATCGT TATCATTCCT TACTTCTTAA ACTTTC          56
75
```

```
154     (2) INFORMATION FOR SEQ ID NO: 6:
155
156         (i) SEQUENCE CHARACTERISTICS:
157             (A) LENGTH: 495 base pairs
158             (B) TYPE: nucleic acid
159             (C) STRANDEDNESS: both
160             (D) TOPOLOGY: unknown
161
162        (ii) MOLECULE TYPE: cDNA
163
164
165        (ix) FEATURE:
166             (A) NAME/KEY: CDS
167             (B) LOCATION: 1..495
168
169
170        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
171
172   TGT GAT CTG CCT CAA ACC CAC AGC CTG GGT AGC AGG AGG ACC TTG ATG       48
173   Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met
174    1               5                  10                  15
175
176   CTC CTG GCA CAG ATG AGG AGA ATC TCT CTT TTC TCC TGC TTG AAG GAC       96
177   Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp
178               20                  25                  30
179
180   AGA CGT GAC TTT GGA TTT CCC CAG GAG GAG TTT GGC AAC CAG TTC CAA      144
181   Arg Arg Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln
182               35                  40                  45
183
```

INPUT SET: S2395.raw

```
184   AAG GCT GAA ACC ATC CCT GTC CTC CAT GAG ATG ATC CAG CAG ATC TTC   192
185   Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe
186        50                  55                  60
187

188   AAT CTC TTC AGC ACA AAG GAC TCA TCT GCT GCT TGG GAT GAG ACC CTC   240
189   Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu
190    65                  70                  75                  80
191

192   CTA GAC AAA TTC TAC ACT GAA CTC TAC CAG CAG CTG AAT GAC CTG GAA   288
193   Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu
194                  85                  90                  95
195

196   GCC TGT GTG ATA CAG GGG GTG GGG GTG ACA GAG ACT CCC CTG ATG AAG   336
197   Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Lys
198                  100                 105                 110
199

200   GAG GAC TCC ATT CTG GCT GTG AGG AAA TAC TTC CAA AGA ATC ACT CTC   384
201   Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu
202                  115                 120                 125
203

204   TAT CTG AAA GAG AAG AAA TAC AGC CCT TGT GCC TGG GAG GTT GTC AGA   432
205   Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg
206        130                 135                 140
207

208   GCA GAA ATC ATG AGA TCT TTT TCT TTG TCA ACA AAC TTG CAA GAA AGT   480
209   Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser
210   145                 150                 155                 160
211

212   TTA AGA AGT AAG GAA                                                495
213   Leu Arg Ser Lys Glu
214                  165
215
216
```

```
261   (2)  INFORMATION FOR SEQ ID NO: 8:
262
263        (i)  SEQUENCE CHARACTERISTICS:
264             (A)  LENGTH: 869 base pairs
265             (B)  TYPE: nucleic acid
266             (C)  STRANDEDNESS: both
267             (D)  TOPOLOGY: unknown
268
269        (ii)  MOLECULE TYPE: cDNA
270
271
272
273        (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 8:
274
275   GAATTCGAGA TTATCGTCAC TGCAATGCTT CGCAATATGG CGCAAAATGA CCAACAGCGG   60
276
277   TTGATTGATC AGGTAGAGGG GGCGCTGTAC GAGGTAAAGC CCGATGCCAG CATTCCTGAC   120
278
279   GACGATACGG AGCTGCTGCG CGATTACGTA AAGAAGTTAT TGAAGCATCC TCGTCAGTAA   180
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```
280
281    AAAGTTAATC TTTTCAACAG CTGTCATAAA GTTGTCACGG CCGAGACTTA TAGTCGCTTT    240
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283    GTTTTTATTT TTTAATGTAT TTGCTCGAGA GGTTGAGGTG ATTTTATGAA AAAGAATATC    300
284
285    GCATTCTTC TTGCATCTAT GTTCGTTTTT TCTATTGCTA CAAATGCCTA TGCATGTGAT     360
286
287    CTGCCTCAAA CCCACAGCCT GGGTAGCAGG AGGACCTTGA TGCTCCTGGC ACAGATGAGG    420
288
289    AGAATCTCTC TTTTCTCCTG CTTGAAGGAC AGACGTGACT TTGGATTTCC CCAGGAGGAG    480
290
291    TTTGGCAACC AGTTCCAAAA GGCTGAAACC ATCCCTGTCC TCCATGAGAT GATCCAGCAG    540
292
293    ATCTTCAATC TCTTCAGCAC AAAGGACTCA TCTGCTGCTT GGGATGAGAC CCTCCTAGAC    600
294
295    AAATTCTACA CTGAACTCTA CCAGCAGCTG AATGACCTGG AAGCCTGTGT GATACAGGGG    660
296
297    GTGGGGGTGA CAGAGACTCC CCTGATGAAG GAGGACTCCA TTCTGGCTGT GAGGAAATAC    720
298
299    TTCCAAAGAA TCACTCTCTA TCTGAAAGAG AAGAAATACA GCCCTTGTGC CTGGGAGGTT    780
300
301    GTCAGAGCAG AAATCATGAG ATCTTTTTCT TTGTCAACAA ACTTGCAAGA AAGTTTAAGA    840
302
303    AGTAAGGAAT GATAACGATC GTAACTGCA                                       869
304
```

```
305    (2)  INFORMATION FOR SEQ ID NO: 9:
306
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308              (A)  LENGTH: 1177 base pairs
309              (B)  TYPE: nucleic acid
310              (C)  STRANDEDNESS: both
311              (D)  TOPOLOGY: unknown
312
313        (ii)  MOLECULE TYPE: cDNA
314
315
316        (ix)  FEATURE:
317              (A)  NAME/KEY: CDS
318              (B)  LOCATION: 286..873
319              (D)  OTHER INFORMATION: /function= "Cytokine"
320                      /product= "Interferon-omega1"
321
322        (ix)  FEATURE:
323              (A)  NAME/KEY: mat_peptide
324              (B)  LOCATION: 355..873
325              (D)  OTHER INFORMATION: /function= "Cytokine"
326                      /product= "Interferon-omega"
327
328        (ix)  FEATURE:
329              (A)  NAME/KEY: sig_peptide
330              (B)  LOCATION: 286..354
331              (D)  OTHER INFORMATION: /product= "ST II Leader"
```

```
332
333
334        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
335
336   GAATTGGAGA TTATCGTCAC TGCAATGCTT CGCAATATGG CGCAAAATGA CCAACAGCGG      60
337
338   TTGATTGATC AGGTAGAGGG GGCGCTGTAC GAGGTAAAGC CCGATGCCAG CATTCCTGAC     120
339
340   GACGATACGG AGCTGCTGCG CGATTACGTA AAGAAGTTAT TGAAGCATCC TCGTCAGTAA     180
341
342   AAAGTTAATC TTTTCAACAG CTGTCATAAA GTTGTCACGG CCGAGACTTA TAGTCGCTTT     240
343
344   GTTTTTATTT TTTAATGTAT TTGCTCGAGA GGTTGAGGTG ATTTT ATG AAA AAG        294
345                                                     Met Lys Lys
346                                                     -23
347
348   AAT ATC GCA TTT CTT CTT GCA TCT ATG TTC GTT TTT TCT ATT GCT ACA      342
349   Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe Ser Ile Ala Thr
350   -20                 -15                 -10                 -5
351
352   AAT GCC TAT GCA TGT GAT CTG CCT CAG AAC CAT GGC CTA CTT AGC AGG      390
353   Asn Ala Tyr Ala Cys Asp Leu Pro Gln Asn His Gly Leu Leu Ser Arg
354                   1               5                   10
355
356   AAC ACC TTG GTG CTT CTG CAC CAA ATG AGG AGA ATC TCC CCT TTC TTG      438
357   Asn Thr Leu Val Leu Leu His Gln Met Arg Arg Ile Ser Pro Phe Leu
358           15                  20                  25
359
360   TGT CTC AAG GAC AGA AGA GAC TTC AGG TTC CCC CAG GAG ATG GTA AAA      486
361   Cys Leu Lys Asp Arg Arg Asp Phe Arg Phe Pro Gln Glu Met Val Lys
362       30                  35                  40
363
364   GGG AGC CAG TTG CAG AAG GCC CAT GTC ATG TCT GTC CTC CAT GAG ATG      534
365   Gly Ser Gln Leu Gln Lys Ala His Val Met Ser Val Leu His Glu Met
366   45                  50                  55                  60
367
368   CTG CAG CAG ATC TTC AGC CTC TTC CAC ACA GAG CGC TCC TCT GCT GCC      582
369   Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser Ser Ala Ala
370                   65                  70                  75
371
372   TGG AAC ATG ACC CTC CTA GAC CAA CTC CAC ACT GGA CTT CAT CAG CAA      630
373   Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr Gly Leu His Gln Gln
374                   80                  85                  90
375
376   CTG CAA CAC CTG GAG ACC TGC TTG CTG CAG GTA GTG GGA GAA GGA GAA      678
377   Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly Glu Gly Glu
378           95                  100                 105
379
380   TCT GCT GGG GCA ATT AGC AGC CCT GCA CTG ACC TTG AGG AGG TAC TTC      726
381   Ser Ala Gly Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg Arg Tyr Phe
382   110                 115                 120
383
384   CAG GGA ATC CGT GTC TAC CTG AAA GAG AAG AAA TAC AGC GAC TGT GCC      774
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INPUT SET: S2395.raw

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386    125             130             135             140
387
388    TGG GAA GTT GTC AGA ATG GAA ATC ATG AAA TCC TTG TTC TTA TCA ACA      822
389    Trp Glu Val Val Arg Met Glu Ile Met Lys Ser Leu Phe Leu Ser Thr
390                        145             150             155
391
392    AAC ATG CAA GAA AGA CTG AGA AGT AAA GAT AGA GAC CTG GGC TCA TCT      870
393    Asn Met Gln Glu Arg Leu Arg Ser Lys Asp Arg Asp Leu Gly Ser Ser
394                   160             165             170
395
396    TGAAATGATT CTCATTGATT AATTTGCCAT ATAACACTTG CACATGTGAC TCTGGTCAAT     930
397
398    TCAAAAGACT CTTATTTCGG CTTTAATCAC AGAATTGACT GAATTAGTTC TGCAAATACT     990
399
400    TTGTCGGTAT ATTAAGCCAG TATATGTTAA AAAGACTTAG GTTCAGGGGC ATCAGTCCCT    1050
401
402    AAGATGTTAT TTATTTTTAC TCATTTATTT ATTCTTACAT TTTATCATAT TTATACTATT    1110
403
404    TATATTCTTA TATAACAAAT GTTTGCCTTT ACATTGTATT AAGATAACAA AACATGTTCA    1170
405
406    GGATCCA                                                             1177
407
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458    (2)  INFORMATION FOR SEQ ID NO: 11:
459
460        (i)  SEQUENCE CHARACTERISTICS:
461             (A)  LENGTH: 879 base pairs
462             (B)  TYPE: nucleic acid
463             (C)  STRANDEDNESS: both
464             (D)  TOPOLOGY: unknown
465
466       (ii)  MOLECULE TYPE: cDNA
467
468
469
470       (ix)  FEATURE:
471             (A)  NAME/KEY: CDS
472             (B)  LOCATION: 286..852
473
474       (ix)  FEATURE:
475             (A)  NAME/KEY: mat_peptide
476             (B)  LOCATION: 355..852
477             (D)  OTHER INFORMATION: /function= "Cytokine"
478                     /product= "Interferon-alpha-2c"
479
480       (ix)  FEATURE:
481             (A)  NAME/KEY: sig_peptide
482             (B)  LOCATION: 286..354
483             (D)  OTHER INFORMATION: /product= "ST II Leader"
484
485
486       (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 11:
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INPUT SET: S2395.raw

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487
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490  TTGATTGATC AGGTAGAGGG GGCGCTGTAC GAGGTAAAGC CCGATGCCAG CATTCCTGAC 120
491
492  GACGATACGG AGCTGCTGCG CGATTACGTA AAGAAGTTAT TGAAGCATCC TCGTCAGTAA 180
493
494  AAAGTTAATC TTTTCAACAG CTGTCATAAA GTTGTCACGG CCGAGACTTA TAGTCGCTTT 240
495
496  GTTTTTATTT TTAATGTAT TTGCTCGAGA GGTTGAGGTG ATTTT ATG AAA AAG      294
497                                                    Met Lys Lys
498                                                    -23
499
500  AAT ATC GCA TTT CTT CTT GCA TCT ATG TTC GTT TTT TCT ATT GCT ACA  342
501  Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe Ser Ile Ala Thr
502  -20                    -15                -10                 -5
503
504  AAT GCC TAT GCA TGT GAT CTG CCT CAA ACC CAC AGC CTG GGT AGC AGG  390
505  Asn Ala Tyr Ala Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg
506                      1             5                   10
507
508  AGG ACC TTG ATG CTC CTG GCA CAG ATG AGG AGA ATC TCT CTT TTC TCC  438
509  Arg Thr Leu Met Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser
510           15                   20                   25
511
512  TGC TTG AAG GAC AGA CGT GAC TTT GGA TTT CCC CAG GAG GAG TTT GGC  486
513. Cys Leu Lys Asp Arg Arg Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly
514           30                   35                   40
515
516  AAC CAG TTC CAA AAG GCT GAA ACC ATC CCT GTC CTC CAT GAG ATG ATC  534
517  Asn Gln Phe Gln Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile
518   45                   50                   55                   60
519
520  CAG CAG ATC TTC AAT CTC TTC AGC ACA AAG GAC TCA TCT GCT GCT TGG  582
521  Gln Gln Ile Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp
522                   65                   70                   75
523
524  GAT GAG ACC CTC CTA GAC AAA TTC TAC ACT GAA CTC TAC CAG CAG CTG  630
525  Asp Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu
526                   80                   85                   90
527
528  AAT GAC CTG GAA GCC TGT GTG ATA CAG GGG GTG GGG GTG ACA GAG ACT  678
529  Asn Asp Leu Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr
530           95                  100                  105
531
532  CCC CTG ATG AAG GAG GAC TCC ATT CTG GCT GTG AGG AAA TAC TTC CAA  726
533  Pro Leu Met Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln
534      110                  115                  120
535
536  AGA ATC ACT CTC TAT CTG AAA GAG AAG AAA TAC AGC CCT TGT GCC TGG  774
537  Arg Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp
538  125                  130                  135                  140
539
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RAW SEQUENCE LISTING
PATENT APPLICATION   *US/08/249,671*

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540   GAG GTT GTC AGA GCA GAA ATC ATG AGA TCT TTT TCT TTG TCA ACA AAC   822
541   Glu Val Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn
542                   145                 150                 155

543

544   TTG CAA GAA AGT TTA AGA AGT AAG GAA TGATAACGAT CGTAACTGCA           869
545   Leu Gln Glu Ser Leu Arg Ser Lys Glu
546               160             165

547

548   GAAGCTTAAT                                                          879

549
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